

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT:
(A) NAME: ZENECA LIMITED
(B) STREET: 15 STANHOPE GATE
(C) CITY: LONDON
(D) STATE: LONDON
(E) COUNTRY: UNITED KINGDOM
(F) POSTAL CODE (ZIP): W1Y 6LN
- (ii) TITLE OF INVENTION: GENETIC CONTROL OF FRUIT RIPENING
- (iii) NUMBER OF SEQUENCES: 57
- (iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
- (v) CURRENT APPLICATION DATA:
APPLICATION NUMBER: GB PPD

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 785 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
(B) CLONE: U-U9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

45	CGGCACGAGG AAAAACTANG TGAGAANGAG ATAATCGTTG ACCGAGGNAG AGAAATGGCGA	60
	GGCGAGAACAG CAAATCCTG ATCATCGGGG GCACCGGGTA CATCGGCAAG TTCATCGTGT	120
50	TTCGGAGGCG CAGGTTAGGT AACCCCTACCT TCGCTCTCGT CCGGAGCACCC ACCGCCCG	180
	CGGCCCAACC CGGAAAGGCC AAGCTCTGGA GCGACTTCCA GGCGCCGGC GTCACCCCTCG	240
55	TCCAGGGGA TATNTATAAC CACCGAGAGTC TGGTAAAGGC GATCAAGCTG GTGGATGTGG	300
	TCATCTCCCC CGTCGGCTTC GGGCANCTGA NTGATCAGAC CAAGATCATC GACGCCATCN	360
60	AANAAGCCGG AGGRCACATC AAGAGGTACC TTCCATCGGA GTTTGGCAAC GACGTANACCC	420
	GAAGCCATGC TGTGGAGCCA GCAAAGTCTA CCTTTGTCGT CAAGCAACAA ATCANAAGGG	480
65	CTGTTGAGGC ATCGGGTNCT CCTTACACCT TTGTATCTTC CAACTTTCTT CGGGGGTNT	540
	TTCCCTCCCGG TATTATGACA GGCGAGGAGC ACTGGTCCTC CCACGGACAA GGTTGTCATC	600
70	TTAGGTTACG GGAACNCAAA ACGATCTCT CNATGAANAC GACTCCGGA CATCCATT	660
	ANTCTTGAT GATCCATAAC CTGAACCAGG TTCTATTTCT TAAACTTCC NCCRCTTCTT	720
75	NTCTCTTANC ANCTCNNTTC CCTCTGGGA AAAAAATGTC NNCTANACTT CNAAAAGGGT	780
	TTTANT	785

(2) INFORMATION FOR SEQ ID NO: 2:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 813 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: cDNA

- 15 (vii) IMMEDIATE SOURCE:
 (B) CLONE: U-U17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

20	CGCGCACGAG GAAAGAAAATC AGGTGAGAAN GAGATAATCG TTGACCCGAGG NAGAGAACATTGG	60
	CGAGCGAGAA GAGCAAAATC CTGATCATCG GGGGCACCCG GTACATCGGC AAGTTCATCG	120
25	TGTTTGCAGG CGCCAGGTTA GGTAACCCCTA CCTTCGCTCT CGTCCGGAGC ACCACCGCCC	180
	CCGCGGCCA ACCCGAGAAC GCAAGCTCC TGAGCGACTT CAAGGCCGCC GGCAGTCACCC	240
30	TCGTCAGGGG GGATATATAT AACCACGAGA GTCTGGTTAA GGCGATCAAG CTGGTGGATG	300
	TGGTCATCTC CCCCGTCGGC TTCCGGGCANC TGANTGATCA GACCAAGATC ATCGACGCCA	360
35	TCAAAGAAGC CGGAGGACAC ATCAAGAGGT ACCTTCCATC GGAGTTTGC AACGACGTAN	420
	ACCGGAAGCCA TGCCTGGAG CCAGCAAAGT CGACCTTTGT CGTCAGGCAA CAAATCANAA	480
40	GGGCTGTTGA GGATCGGGAT ATCCCTTACA CCTTTGATTC TTCCAACCTTC TTCGGTGGGT	540
	NTTTCCCTCCC GGATTATTANGA CAGGCAGGAG CCACTGGTCC TCCCACGGAC AAGGTTGTCA	600
45	TCTTANGTGA CGGGAACACAA AAAGCGATCT TTCTCAATGA ANACACATCC GGACNTNCAC	660
	NATTAAAGCA GTGGATGATC CGAAAACCTG AACANGTTCT ATATCTGAAA CCTTCGCCA	720
	CTCTTGTCCTC ATNACAACTC ATTTCCCTCT GGAAAAAAA NGTCNGCAA ACTCCNAAA	780
	GGTCTACTTC CGCGAAGAAA AATCTGAANC ANA	813

(2) INFORMATION FOR SEQ ID NO: 3:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 746 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

55 (ii) MOLECULE TYPE: cDNA

- 60 (vii) IMMEDIATE SOURCE:
 (B) CLONE: U-U66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

65	GGCACGAGGG GAAAAGGAGA TNATCGTTGA CGGAGGAGAG AATGGCGAGC GAGAAGAGCA	60
	AGATCCTGAT CATCGGGGGC ACGGGGTACA TCGGCAAGTT CATCGTGTGTT GCGAGGCCA	120
70	GGTTAGGTAA CCCTACCTTC GCTCTCGTCC GGAGCACCAC CGCCCCCGCC GGCCAACCCG	180

	AGAAGGGCAA GCTCCTGAGC GACTTCCAGG CGCCGGCGT CACCCCTGGTC CAGGGGGATA	240
	TATATAACCA CNAGAGTCTG GTTAAGGCRA TCAAGCTGGT GGATGTGGTC ATCTCCCCG	300
5	TGGCCTTCGG GCAGCTGAGT GATCAGACTA AGATCATCGA CGCCATCAAA GAAAGCCGGA	360
	GGCACATCA AGAGGTACCT TCCATCGGGA GTTGGCAAC GACGTANACC AAAGCCATGC	420
10	TGTGGAAGCC ANCAAAGTCG ACCTTTGTCG TCAAGCAACA AATTANAAGG GCTGTTGAGG	480
	CATCGGGGAT CCCTTACACC TTGTTATCT TCCAACCTCT TCGGTGGGT A TNTCTCCCC	540
	GTATTGGGAC AGGCANGAAC CACTGGCTC CCCACGGAC AAGGTTGTCN TCTTAGGTGA	600
15	ACGGGAACAC CAANGCGATC TTCTCAATG AAAGACAAC T CGGGACATNC CCACTTAAAC	660
	CANTGGGATGA TCCNANAACC TGAAACAAGGT CTATTTCTGA AAACCTCNCC ATCTTCTTT	720
20	TCTCATAACG AACCCNTTT CCTCTT	746

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 795 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (B) CLONE: U-U104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

	GGCACGAGGA AANAGATAA TCGTTGACCG AGGCAGAGAA TGGCGAGCGA GAAGAGCAAA	60
	ATCCCTGATCA TCGGGGGCAC CGGGTACATC GGCAAGTTCA TCGTGTGTTGC GAGCGCCAGG	120
	TTAGGTAACC CTACCTTCGC TCTCGTCCGG AGCACCCACCG CCCCCGCCGG CCAACCCGAG	180
45	AAGGCCAACG TCCTGAGCGA CTTCAGGCC GCGGGCGTC ACCTCGTCCA GGGGGATATA	240
	TATAACCACG AGACTCTGGT TAAGGGGATC AAGCTGGGG ATGTGGTCAT CTCCCCGGTC	300
	GGCTTCGGGC AGCTGACTGA TCAAGACCAAG ATCATCGACG CCATCAAAGA AGCCGGAGGA	360
	CACATCAAGA GGTACCTTCC ATCGGGAGTT TGGCAACGAC GTTANACCGA AGCCATGCTG	420
	TGGAGGCCAGC AAAGTCNACC TTGTCGTC AGCAACAAAT CANAAGGGCT GTTGANGCAT	480
55	CGGGTNTCCC TTACACCTTT GTATCTTCA ACTCTTCGG TGGGTATTC CTCCCGGTAT	540
	TANGACAGGC AGGACCACTG GTCTTCCCCA CNGACAAGGT TGTCNTCTTA GTGACNGGA	600
	ACACAAAANC ATCTTCTCN ATGAAGACAA CTCCGGACAT ACNCNATTAA AGCNGTGGAT	660
60	GATCCCCAAA CCTGAACAAG TTCTCATNTC TTGAAAACCTT TCCCGCCCAA CCATCTTTN	720
	GTTCCTCCNT TAAACCNAC A CTCCATTTC CCCTCCTGG GGAAAAAAA AAGGTCCGGC	780
65	NAANAACCTTC CNAAA	795

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS: